

IN THE CLAIMS

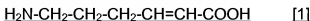
This listing of claims replaces all prior versions, and listings, in this application.

1. (original) Process for the biochemical synthesis of 6-amino caproic acid wherein either 6-amino-hex-2-enoic acid of formula [1] (6-AHEA)



or wherein 6-amino-2-hydroxy-hexanoic acid (6-AHHA), a compound capable of being transformed into 6-amino-hex-2-enoic acid, is treated with an enzyme having α,β -enoate reductase activity towards molecules containing an α,β -enoate group and a primary amino group, in particular with an enzyme having α,β -enoate reductase activity towards 6-amino-hex-2-enoic acid.

2. (currently amended) Process for the biochemical synthesis of 6-amino caproic acid wherein either 6-amino-hex-2-enoic acid of formula [1] (6-AHEA)



or 6-amino-2-hydroxy-hexanoic acid (6-AHHA), a compound capable of being transformed into 6-amino-hex-2-enoic acid, is treated with an enzyme having α,β -enoate reductase activity towards molecules containing an α,β -enoate group and a primary amino group ~~according to one of claims 4~~, characterized in that the enzyme having α,β -enoate reductase activity is an enzyme originating from a microorganism selected from the group consisting of species of *Acetobacterium* sp., *Acremonium* sp., *Agrobacterium* sp., *Burkholderia* sp., *Cephalosporium* sp., *Clostridium* sp., *Escherichia* sp., *Moorella* sp., *Ochrobactrum* sp., *Pseudomonas* sp., *Salmonella* sp., *Shigella* sp., *Tilachlidium* sp., *Yersinia* sp., and *Vibrio* sp.

3. (currently amended) Process for the biochemical synthesis of 6-amino caproic acid wherein either 6-amino-hex-2-enoic acid of formula [1] (6-AHEA)



or 6-amino-2-hydroxy-hexanoic acid (6-AHHA), a compound capable of being transformed into 6-amino-hex-2-enoic acid, is treated with an enzyme having α,β -enoate reductase activity towards molecules containing an α,β -enoate group and a primary

amino group according to one of claims 4, characterized in that the enzyme having α,β -enoate reductase activity is an enzyme originating from *Acremonium* sp., *Clostridium* sp., *Moorella* sp. or *Ochrobactrum* sp.

4. (previously presented) Process according to claim 3, characterized in that the enzyme having α,β -enoate reductase activity is an enzyme from *Acremonium strictum* CBS114157, *Clostridium tyrobutyricum* DSM1460, *Moorella thermoacetica* DSM1974, *Ochrobactrum anthropi* NCIMB41200, or *Clostridium kluyveri* DSM555.

5. (currently amended) Process for the biochemical synthesis of 6-amino caproic acid wherein either 6-aminohex-2-enoic acid of formula [1] (6-AHEA)



or 6-amino-2-hydroxy-hexanoic acid (6-AHHA), a compound capable of being transformed into 6-aminohex-2-enoic acid, is treated with an enzyme having α,β -enoate reductase activity towards molecules containing an α,β -enoate group and a primary amino group according to one of claims 4, characterized in that the enzyme having α,β -enoate reductase activity has aerostable α,β -enoate reductase activity and is an enzyme originating from a microorganism selected from the group consisting of species of *Agrobacterium* sp., *Burkholderia* sp., *Escherichia* sp., *Pseudomonas* sp., *Salmonella* sp., *Shigella* sp., *Yersinia* sp., and *Vibrio* sp.

6. (currently amended) Process for the biochemical synthesis of 6-amino caproic acid wherein either 6-aminohex-2-enoic acid of formula [1] (6-AHEA)



or 6-amino-2-hydroxy-hexanoic acid (6-AHHA), a compound capable of being transformed into 6-aminohex-2-enoic acid, is treated with an enzyme having aerostable α,β -enoate reductase activity towards molecules containing an α,β -enoate group and a primary amino group according to one of claims 5, characterized in that the enzyme having aerostable α,β -enoate reductase activity is an enzyme originating from an *Escherichia coli* species.

7. (previously presented) Process according to claim 6, characterized in that the enzyme having aerostable α,β -enoate reductase activity is an enzyme originating from *Escherichia coli* K12.
8. (previously presented) Process according to claim 1, characterized in that 6-aminohept-2-enoic acid is being converted into 6-amino caproic acid at a pH in the range from 3 to 9.
9. (previously presented) Process according to claim 8, characterized in that the pH is in the range of from 4 to 8.
10. (original) Process according to claim 9, characterized in that the pH is in the range of from 5 to 8.
11. (previously presented) Process according to claim 8, characterized in that the pH is in the range of from 5.5 to 7 under anaerobic conditions or of from 6.5 to 8 under aerobic conditions.
12. (previously presented) Process according to claim 1, characterized in that the process is carried out in a host organism selected from the group consisting of genera of *Aspergillus*, *Bacillus*, *Corynebacterium*, *Escherichia* and *Pichia*.
13. (previously presented) Process according to claim 12, characterized in that the process is carried out in a host organism selected from the group consisting of *Escherichia coli*, *Bacillus*, *Corynebacterium glutamicum*, *Aspergillus niger* and *Pichia pastoris* host organisms.
14. (previously presented) Process according to claim 12, characterized in that in the host organism an α,β -enoate reductase gene encoding an enzyme having α,β -enoate reductase activity towards molecules containing an α,β -enoate group and a primary amino group is cloned and expressed.

Claims 15-27 (canceled)

28. (new) A process for biochemically synthesizing 6-amino caproic acid, the process comprising treating 6-aminohex-2-enoic acid of formula [1] (6-AHEA)



with an enzyme having α,β -enoate reductase activity towards molecules containing an α,β -enoate group and a primary amino group to synthesize 6-amino caproic acid.

29. (new) The process according to claim 28, wherein the enzyme having α,β -enoate reductase activity is an enzyme originating from a microorganism selected from the group consisting of species of *Acetobacterium* sp., *Acremonium* sp., *Agrobacterium* sp., *Burkholderia* sp., *Cephalosporium* sp., *Clostridium* sp., *Escherichia* sp., *Moorella* sp., *Ochrobactrum* sp., *Pseudomonas* sp., *Salmonella* sp., *Shigella* sp., *Tilachlidium* sp., *Yersinia* sp., and *Vibrio* sp.

30. (new) The process according to claim 28, wherein the enzyme having α,β -enoate reductase activity is an enzyme originating from *Acremonium* sp., *Clostridium* sp., *Moorella* sp., or *Ochrobactrum* sp.

31. (new) The process according to claim 30, wherein the enzyme having α,β -enoate reductase activity is an enzyme from *Acremonium strictum* CBS114157, *Clostridium tyrobutyricum* DSM1460, *Moorella thermoacetica* DSM1974, *Ochrobactrum anthropi* NCIMB41200, or *Clostridium kluyveri* DSM555.

32. (new) The process according to claim 28, wherein the enzyme having α,β -enoate reductase activity has aerostable α,β -enoate reductase activity and is an enzyme originating from a microorganism selected from the group consisting of species of *Agrobacterium* sp., *Burkholderia* sp., *Escherichia* sp., *Pseudomonas* sp., *Salmonella* sp., *Shigella* sp., *Yersinia* sp., and *Vibrio* sp.

33. (new) The process according to claim 32, wherein the enzyme having aerostable α,β -enoate reductase activity is an enzyme originating from an *Escherichia coli* species.
34. (new) The process according to claim 28, wherein 6-aminohept-2-enoic acid is being converted into 6-amino caproic acid at a pH in the range from 3 to 9.
35. (new) The process according to claim 34, wherein the pH is in the range of from 4 to 8.
36. (new) The process according to claim 35, wherein the pH is in the range of from 5 to 8.
37. (new) The process according to claim 34, wherein the pH is in the range of from 5.5 to 7 under anaerobic conditions or of from 6.5 to 8 under aerobic conditions.
38. (new) The process according to claim 28, wherein the process is carried out in a host organism selected from the group consisting of genera of *Aspergillus*, *Bacillus*, *Corynebacterium*, *Escherichia*, and *Pichia*.
39. (new) The process according to claim 38, wherein the process is carried out in a host organism selected from the group consisting of *Escherichia coli*, *Bacillus*, *Corynebacterium glutamicum*, *Aspergillus niger*, and *Pichia pastoris* host organisms.
40. (new) The process according to claim 38, wherein the host organism an α,β -enoate reductase gene encoding an enzyme having α,β -enoate reductase activity towards molecules containing an α,β -enoate group and a primary amino group is cloned and expressed.